

4121-126_third_submission.ST25 SEQUENCE LISTING	
<110> Breitling, Frank Poustka, Annemarie Moldenhauer, Gerhard	
<120> SELECTION OF MONOCLONAL ANTIBODIES	
<130> 4121-126	
<140> US 09/889,182 <141> 2001-07-10	
<150> PCT/DE00/00079 <151> 2000-01-11	
<160> 8	
<170> PatentIn version 3.2	
<210> 1 <211> 5732 <212> DNA <213> Artificial Sequence	
<220> <223> Synthetic sequence	
<220> <221> CDS <222> (737)(1420)	
<400> 1 gcgcgcgttg acattgatta ttgactagtt attaatagta atcaattacg gggtcattag	60
ttcatagccc atatatggag ttccgcgtta cataacttac ggtaaatggc ccgcctggct	120
gaccgcccaa cgacccccgc ccattgacgt caataatgac gtatgttccc atagtaacgc	180
caatagggac tttccattga cgtcaatggg tggactattt acggtaaact gcccacttgg	240
cagtacatca agtgtatcat atgccaagta cgccccctat tgacgtcaat gacggtaaat	300
ggcccgcctg gcattatgcc cagtacatga ccttatggga ctttcctact tggcagtaca	360
tctacgtatt agtcatcgct attaccatgg tgatgcggtt ttggcagtac atcaatgggc	420
gtggatagcg gtttgactca cggggatttc caagtctcca ccccattgac gtcaatggga	480
gtttgttttg gcaccaaaat caacgggact ttccaaaatg tcgtaacaac tccgcccat	540
tgacgcaaat gggcggtagg cgtgtacggt gggaggtcta tataagcaga gctctctggc	600
taactagaga acccactgct tactggctta tcgaaattaa tacgactcac tatagggaga	660
cccaagcttg gtaccgagct cggatccact agtaacggcc gccagtgtgc tggaattcgg	720
cttggggata tccacc atg gag aca gac aca ctc ctg cta tgg gta ctg ctg Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu 1 5 10	772
ctc tgg gtt cca ggt tcc act ggt gac tat cca tat gat gtt cca gat Leu Trp Val Pro Gly Ser Thr Gly Asp Tyr Pro Tyr Asp Val Pro Asp 15 20 25	820
tat gct ggg gcc caa aag ccc gag gtg atc gat gcc agc gag ctg acc Tyr Ala Gly Ala Gln Lys Pro Glu Val Ile Asp Ala Ser Glu Leu Thr 30 35 40	868

4121-126_third_submission.ST25 ccc gcc gtg acc acc tac aag cta gtg atc aac ggc aag acc ctg aag Pro Ala Val Thr Thr Tyr Lys Leu Val Ile Asn Gly Lys Thr Leu Lys 45 50 55 60	916
ggc gag acc acc acc gag gcc gtg gac gcc gcc acc gcg gag aag gtg Gly Glu Thr Thr Thr Glu Ala Val Asp Ala Ala Thr Ala Glu Lys Val 65 70 75	964
ttc aaa caa tac gct aat gac aac ggg gtc gac ggc gag tgg act tac Phe Lys Gln Tyr Ala Asn Asp Asn Gly Val Asp Gly Glu Trp Thr Tyr 80 85	1012
gac gac gcc acc aag acc ttc acc gtg acc gag aag ccc gag gtg atc Asp Asp Ala Thr Lys Thr Phe Thr Val Thr Glu Lys Pro Glu Val Ile 95 100 105	1060
gat gcc agc gag ctg acc ccc gcc gtg acc acc tac aag cta gtg atc Asp Ala Ser Glu Leu Thr Pro Ala Val Thr Thr Tyr Lys Leu Val Ile 110 115 120	1108
aac ggc aag acc ctg aag ggc gag acc acc acc gag gcc gtg gac gcc Asn Gly Lys Thr Leu Lys Gly Glu Thr Thr Thr Glu Ala Val Asp Ala 125 130 135 140	1156
gcc acc gcg gag aag gtg ttc aaa caa tac gct aat gac aac ggg gtc Ala Thr Ala Glu Lys Val Phe Lys Gln Tyr Ala Asn Asp Asn Gly Val 145 150 155	1204
gac ggc gag tgg act tac gac gac gcc acc aag acc ttc acc gtg acc Asp Gly Glu Trp Thr Tyr Asp Asp Ala Thr Lys Thr Phe Thr Val Thr 160 165 170	1252
gag gcg gcc gca gaa caa aaa ctc atc tca gaa gag gat ctg aat ggg Glu Ala Ala Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Gly 175 180 185	1300
gcc gtc gac gga caa aac gac acc agc caa acc agc ag	1348
tcc agc aac ata agc gga ggc att ttc ctt ttc ttc gtg gcc aat gcc Ser Ser Asn Ile Ser Gly Gly Ile Phe Leu Phe Phe Val Ala Asn Ala 205 210 215 220	1396
ata atc cac ctc ttc tgc ttc agt tgaggtgaca cgtctagagc tattctatag Ile Ile His Leu Phe Cys Phe Ser 225	1450
tgtcacctaa atgctagagc tcgctgatca gcctcgactg tgccttctag ttgccagcca	1510
tctgttgttt gcccctcccc cgtgccttcc ttgaccctgg aaggtgccac tcccactgtc	1570
ctttcctaat aaaatgagga aattgcatcg cattgtctga gtaggtgtca ttctattctg	1630
gggggtgggg tggggcagga cagcaagggg gaggattggg aagacaatag caggcatgct	1690
ggggatgcgg tgggctctat ggcttctgag gcggaaagaa ccagtggcgg taatacggtt	1750
atccacagaa tcaggggata acgcaggaaa gaacatgtga gcaaaaggcc agcaaaaggc	1810
caggaaccgt aaaaaggccg cgttgctggc gtttttccat aggctccgcc cccctgacga	1870
gcatcacaaa aatcgacgct caagtcagag gtggcgaaac ccgacaggac tataaagata	1930
ccaggcgttt ccccctggaa gctccctcgt gcgctctcct gttccgaccc tgccgcttac	1990
cggatacctg tccgcctttc tcccttcggg aagcgtggcg ctttctcata gctcacgctg	2050
taggtatctc agttcggtgt aggtcgttcg ctccaagctg ggctgtgtgc acgaaccccc	2110

		4	121 126 +bi	rd_submissi	on ST25	
cgttcagccc	gaccgctgcg	ccttatccgg	taactatcgt	cttgagtcca	acccggtaag	2170
acacgactta	tcgccactgg	cagcagccac	tggtaacagg	attagcagag	cgaggtatgt	2230
aggcggtgct	acagagttct	tgaagtggtg	gcctaactac	ggctacacta	gaaggacagt	2290
atttggtatc	tgcgctctgc	tgaagccagt	taccttcgga	aaaagagttg	gtagctcttg	2350
atccggcaaa	caaaccaccg	ctggtagcgg	tggtttttt	gtttgcaagc	agcagattac	2410
gcgcagaaaa	aaaggatctc	aagaagatcc	tttgatcttt	tctacggggt	ctgacgctca	2470
gtggaacgaa	aactcacgtt	aagggatttt	ggtcatgaga	ttatcaaaaa	ggatcttcac	2530
ctagatcctt	ttaaattaaa	aatgaagttt	taaatcaatc	taaagtatat	atgagtaacc	2590
tgaggctatg	gcagggcctg	ccgccccgac	gttggctgcg	agccctgggc	cttcacccga	2650
acttgggggg	tggggtgggg	aaaaggaaga	aacgcgggcg	tattggcccc	aatggggtct	2710
cggtggggta	tcgacagagt	gccagccctg	ggaccgaacc	ccgcgtttat	gaacaaacga	2770
cccaacaccg	tgcgttttat	tctgtctttt	tattgccgtc	atagcgcggg	ttccttccgg	2830
tattgtctcc	ttccgtgttt	cagttagcct	ccccctaggg	tgggcgaaga	actccagcat	2890
gagatccccg	cgctggagga	tcatccagcc	ggcgtcccgg	aaaacgattc	cgaagcccaa	2950
cctttcatag	aaggcggcgg	tggaatcgaa	atctcgtgat	ggcaggttgg	gcgtcgcttg	3010
gtcggtcatt	tcgaacccca	gagtcccgct	cagaagaact	cgtcaagaag	gcgatagaag	3070
gcgatgcgct	gcgaatcggg	agcggcgata	ccgtaaagca	cgaggaagcg	gtcagcccat	3130
tcgccgccaa	gctcttcagc	aatatcacgg	gtagccaacg	ctatgtcctg	atagcggtcc	3190
gccacaccca	gccggccaca	gtcgatgaat	ccagaaaagc	ggccattttc	caccatgata	3250
ttcggcaagc	aggcatcgcc	atgggtcacg	acgagatcct	cgccgtcggg	catgctcgcc	3310
ttgagcctgg	cgaacagttc	ggctggcgcg	agcccctgat	gctcttgatc	atcctgatcg	3370
acaagaccgg	cttccatccg	agtacgtgct	cgctcgatgc	gatgtttcgc	ttggtggtcg	3430
aatgggcagg	tagccggatc	aagcgtatgc	agccgccgca	ttgcatcagc	catgatggat	3490
actttctcgg	caggagcaag	gtgagatgac	aggagatcct	gccccggcac	ttcgcccaat	3550
agcagccagt	cccttcccgc	ttcagtgaca	acgtcgagca	cagctgcgca	aggaacgccc	3610
gtcgtggcca	gccacgatag	ccgcgctgcc	tcgtcttgca	gttcattcag	ggcaccggac	3670
aggtcggtct	tgacaaaaag	aaccgggcgc	ccctgcgctg	acagccggaa	cacggcggca	3730
tcagagcagc	cgattgtctg	ttgtgcccag	tcatagccga	atagcctctc	cacccaagcg	3790
gccggagaac	ctgcgtgcaa	tccatcttgt	tcaatcatgc	gaaacgatcc	tcatcctgtc	3850
tcttgatcga	tctttgcaaa	agcctaggcc	tccaaaaaag	cctcctcact	acttctggaa	3910
tagctcagag	gccgaggagg	cggcctcggc	ctctgcataa	ataaaaaaaa	ttagtcagcc	3970
atggggcgga	gaatgggcgg	aactgggcgg	agttaggggc	gggatgggcg	gagttagggg	4030
cgggactatg	gttgctgact	aattgagatg	catgctttgc	atacttctgc	ctgctgggga	4090
gcctggggac	tttccacacc	tggttgctga	ctaattgaga	tgcatgcttt	gcatacttct	4150
gcctgctggg	gagcctgggg	actttccaca	ccctaactga	cacacattcc	acagctggtt	4210

```
4121-126_third_submission.ST25
                                                                     4270
ctttccgcct caggactctt cctttttcaa taaatcaatc taaagtatat atgagtaaac
                                                                     4330
ttggtctgac agttaccaat gcttaatcag tgaggcacct atctcagcga tctgtctatt
                                                                     4390
tcgttcatcc atagttgcct gactccccgt cgtgtagata actacgatac gggagggctt
                                                                     4450
accatctggc cccagtgctg caatgatacc gcgagaccca cgctcaccgg ctccagattt
                                                                     4510
atcagcaata aaccagccag ccggaagggc cgagcgcaga agtggtcctg caactttatc
                                                                     4570
cgcctccatc cagtctatta attgttgccg ggaagctaga gtaagtagtt cgccagttaa
                                                                     4630
tagtttgcgc aacgttgttg ccattgctac aggcatcgtg gtgtcacgct cgtcgtttgg
                                                                     4690
tatggcttca ttcagctccg gttcccaacg atcaaggcga gttacatgat cccccatgtt
                                                                     4750
gtgcaaaaaa gcggttagct ccttcggtcc tccgatcgtt gtcagaagta agttggccgc
                                                                     4810
agtgttatca ctcatggtta tggcagcact gcataattct cttactgtca tgccatccgt
                                                                     4870
aagatgcttt tctgtgactg gtgagtactc aaccaagtca ttctgagaat agtgtatgcg
gcgaccgagt tgctcttgcc cggcgtcaat acgggataat accgcgccac atagcagaac
                                                                     4930
tttaaaagtg ctcatcattg gaaaacgttc ttcggggcga aaactctcaa ggatcttacc
                                                                     4990
gctgttgaga tccagttcga tgtaacccac tcgtgcaccc aactgatctt cagcatcttt
                                                                     5050
                                                                     5110
tactttcacc agcgtttctg ggtgagcaaa aacaggaagg caaaatgccg caaaaaaggg
                                                                     5170
aataagggcg acacggaaat gttgaatact catactcttc ctttttcaat attattgaag
catttatcag ggttattgtc tcatgagcgg atacatattt gaatgtattt agaaaaataa
                                                                     5230
                                                                     5290
acaaataggg gttccgcgca catttccccg aaaagtgcca cctgacgcgc cctgtagcgg
                                                                     5350
cgcattaagc gcggcgggtg tggtggttac gcgcagcgtg accgctacac ttgccagcgc
cctagcgccc gctcctttcg ctttcttccc ttcctttctc gccacgttcg ccggctttcc
                                                                     5410
                                                                     5470
ccgtcaagct ctaaatcggg ggctcccttt agggttccga tttagtgctt tacggcacct
                                                                     5530
cgaccccaaa aaacttgatt agggtgatgg ttcacgtagt gggccatcgc cctgatagac
                                                                     5590
ggtttttcgc cctttgacgt tggagtccac gttctttaat agtggactct tgttccaaac
tggaacaaca ctcaacccta tctcggtcta ttcttttgat ttataaggga ttttgccgat
                                                                     5650
                                                                     5710
ttcggcctat tggttaaaaa atgagctgat ttaacaaaaa tttaacgcga attttaacaa
                                                                     5732
aatattaacg cttacaattt ac
       2
228
<210>
       PRT
       Artificial Sequence
<220>
<223> Synthetic Construct
<400> 2
Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro 1 	ext{15}
```

Gly Ser Thr Gly Asp Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Gly Ala 20 25 30

Gln Lys Pro Glu Val Ile Asp Ala Ser Glu Leu Thr Pro Ala Val Thr 35 40 45

Thr Tyr Lys Leu Val Ile Asn Gly Lys Thr Leu Lys Gly Glu Thr Thr 50 60

Thr Glu Ala Val Asp Ala Ala Thr Ala Glu Lys Val Phe Lys Gln Tyr 65 70 75 80

Ala Asn Asp Asn Gly Val Asp Gly Glu Trp Thr Tyr Asp Asp Ala Thr 85 90 95

Lys Thr Phe Thr Val Thr Glu Lys Pro Glu Val Ile Asp Ala Ser Glu 100 105 110

Leu Thr Pro Ala Val Thr Thr Tyr Lys Leu Val Ile Asn Gly Lys Thr 115 120 125

Leu Lys Gly Glu Thr Thr Thr Glu Ala Val Asp Ala Ala Thr Ala Glu 130 135 140

Lys Val Phe Lys Gln Tyr Ala Asn Asp Asn Gly Val Asp Gly Glu Trp 145 150 155

Thr Tyr Asp Asp Ala Thr Lys Thr Phe Thr Val Thr Glu Ala Ala Ala 165 170 175

Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Gly Ala Val Asp Gly 180 185 190

Gln Asn Asp Thr Ser Gln Thr Ser Ser Pro Ser Ala Ser Ser Asn Ile 195 200 205

Ser Gly Gly Ile Phe Leu Phe Phe Val Ala Asn Ala Ile Ile His Leu 210 215 220

Phe Cys Phe Ser

<210> 3 <211> 6094

<211> 0094 <212> DNA

<213> Artificial Sequence

<220> <223> Synthetic Sequence

<220> <221> CDS <222> (68

<222> (682)..(1782)

<400> 3
gcgcgcgttg acattgatta ttgactagtt attaatagta atcaattacg gggtcattag
ttcatagccc atatatggag ttccgcgtta cataacttac ggtaaatggc ccgcctggct
Page 5

120

gaccgcccaa	cgacccccg	c ccatto	gacgt ca	ataatgac	gtatgtt	cc ata	gtaacgc	180
caatagggac	tttccattg	a cgtcaa	atggg tg	gactattt	acggtaaa	act gcc	cacttgg	240
cagtacatca	agtgtatca	t atgcca	aagta cg	cccctat	tgacgtca	at gac	ggtaaat	300
ggcccgcctg	gcattatgc	c cagta	catga co	ttatggga	ctttccta	ict tgg	cagtaca	360
tctacgtatt	agtcatcgc	t attac	catgg tg	atgcggtt	ttggcagt	ac atc	aatgggc	420
gtggatagcg	gtttgactc	a cgggga	atttc ca	agtctcca	ccccatto	gac gtc	aatggga	480
gtttgttttg	gcaccaaaa [.]	t caacg	ggact tt	ccaaaatg	tcgtaaca	ac tcc	gccccat	540
tgacgcaaat	gggcggtag	g cgtgta	acggt gg	gaggtcta	tataagca	aga gct	ctctggc	600
taactagaga	acccactgc	t tactg	gctta to	gaaattaa	tacgacto	ac tat	agggaga	660
cccaagcttg	gtaccggtg	c g atg Met 1	gca ccc Ala Pro	tgc atg Cys Met 5	ctg ctc Leu Leu	ctg ct Leu Le	g ttg u Leu 10	711
gcg gcc gcc Ala Ala Ala	ctg gcc Leu Ala 15	ccg act Pro Thr	cag acc Gln Thr	cgc gcg Arg Ala 20	ggg gcc Gly Ala	caa aa Gln Ly 25	g gag s Glu	759
aag acc ccc Lys Thr Pro	gag gag Glu Glu 30	ccc aag Pro Lys	gag gag Glu Glu 35	gtg acc Val Thr	atc aag Ile Lys	gcc aa Ala As 40	c ctg n Leu	807
atc tac gcc Ile Tyr Ala 45	gac ggc Asp Gly	aag acc Lys Thr	cag acc Gln Thr 50	gcc gag Ala Glu	ttc aag Phe Lys 55	ggc ac Gly Th	c ttc r Phe	855
gag gag gcc Glu Glu Ala 60	acc gcg Thr Ala	gag gcc Glu Ala 65	tac cgc Tyr Arg	tac gcc Tyr Ala	gac gcc Asp Ala 70	ctg aa Leu Ly	g aag s Lys	903
gac aac ggc Asp Asn Gly 75	gag tac Glu Tyr	acc gtg Thr Val 80	gac gtg Asp Val	gcc gac Ala Asp 85	aag ggc Lys Gly	tac ac Tyr Th	c ctg r Leu 90	951
aac atc aag Asn Ile Lys	ttc gcc Phe Ala 95	ggc aag Gly Lys	gag aag Glu Lys	acc ccc Thr Pro 100	gag gag Glu Glu	ccc aa Pro Ly 10	s Glu	999
gag gtg acc Glu Val Thr	atc aag Ile Lys 110	gcc aac Ala Asn	ctg ato Leu Ile 115	Tyr Āla	gac ggc Asp Gly	aag ac Lys Th 120	c cag r Gln	1047
acc gcc gag Thr Ala Glu 125	ttc aag	ggc acc Gly Thr	ttc gag Phe Glu 130	gag gcc Glu Ala	acc gcg Thr Ala 135	gag gc Glu Al	c tac a Tyr	1095
cgc tac gcc Arg Tyr Ala 140	gac gcc Asp Ala	ctg aag Leu Lys 145	aag gad Lys Asp	aac ggc Asn Gly	gag tac Glu Tyr 150	acc gt Thr Va	g gac 1 Asp	1143
gtg gcc gac Val Ala Asp 155	Lyš Ğly	tac acc Tyr Thr 160	ctg aac Leu Asn	atc aag Ile Lys 165	ttc gcc Phe Ala	ggc aa Gly Ly	g gag s Glu 170	1191
aag acc ccc Lys Thr Pro	gag gag Glu Glu 175	ccc aag Pro Lys	gag gag Glu Glu	gtg acc Val Thr 180	atc aag Ile Lys	gcc aa Ala As 18	c ctg n Leu 5	1239
atc tac gcc Ile Tyr Ala	gac ggc Asp Gly 190	aag acc Lys Thr	cag acc Gln Thr 195	Ala Glu	ttc aag Phe Lys Page 6	ggc ac Gly Th 200	c ttc r Phe	1287

	gag Glu	gag Glu	gcc Ala 205	acc Thr	gcg Ala	gag Glu	gcc Ala	tac Tyr 210	cgc Arg	tac Tyr	gcc Ala	gac Asp	gcc Ala 215	ctg Leu	aag Lys	aag Lys	1335
,	gac Asp	aac Asn 220	ggc Gly	gag Glu	tac Tyr	acc Thr	gtg Val 225	gac Asp	gtg val	gcc Ala	gac Asp	aag Lys 230	ggc Gly	tac Tyr	acc Thr	ctg Leu	1383
,	aac Asn 235	atc Ile	aag Lys	ttc Phe	gcc Ala	ggc Gly 240	aag Lys	gag Glu	aag Lys	acc Thr	ccc Pro 245	gag Glu	gag Glu	ccc Pro	aag Lys	gag Glu 250	1431
•	gag Glu	gtg Val	acc Thr	atc Ile	aag Lys 255	gcc Ala	aac Asn	ctg Leu	atc Ile	tac Tyr 260	gcc Ala	gac Asp	ggc Gly	aag Lys	acc Thr 265	cag Gln	1479
-	acc Thr	gcc Ala	gag Glu	ttc Phe 270	aag Lys	ggc Gly	acc Thr	ttc Phe	gag Glu 275	gag Glu	gcc Ala	acc Thr	gcg Ala	gag Glu 280	gcc Ala	tac Tyr	1527
,	cgc Arg	tac Tyr	gcc Ala 285	gac Asp	gcc Ala	ctg Leu	aag Lys	aag Lys 290	gac Asp	aac Asn	ggc Gly	gag Glu	tac Tyr 295	acc Thr	gtg val	gac Asp	1575
,	gtg Val	gcc Ala 300	gac Asp	aag Lys	ggc Gly	tac Tyr	acc Thr 305	ctg Leu	aac Asn	atc Ile	aag Lys	ttc Phe 310	gcc Ala	ggc Gly	gcg Ala	gcc Ala	1623
	gca Ala 315	gaa Glu	caa Gln	aaa Lys	ctc Leu	atc Ile 320	tca Ser	gaa Glu	gag Glu	gat Asp	ctg Leu 325	aat Asn	ggg Gly	gcc Ala	gtc val	gac Asp 330	1671
,	gga Gly	caa Gln	aac Asn	gac Asp	acc Thr 335	agc Ser	caa Gln	acc Thr	agc Ser	agc Ser 340	ccc Pro	tca Ser	gca Ala	tcc Ser	agc Ser 345	aac Asn	1719
	ata Ile	agc Ser	gga Gly	ggc Gly 350	att Ile	ttc Phe	ctt Leu	ttc Phe	ttc Phe 355	gtg val	gcc Ala	aat Asn	gcc Ala	ata Ile 360	atc Ile	cac His	1767
				ttc Phe		tga	ggtga	aca (gtc1	tagag	gc ta	attci	tata	g tg	tcac	ctaa	1822
	atgo	taga	agc 1	tcgc	tgate	ca go	ctc	gacto	g tgo	ctt	ctag	ttg	ccag	ca	tctg	ttgttt	1882
,	gcco	ctc	ccc (cgtg	cctt	cc t	tgac	ctg	g aag	ggtg	ccac	tcc	cact	gtc	cttt	cctaat	1942
	aaaa	atgag	gga i	aatt	gcate	cg ca	attg	tctga	a gta	aggt	gtca	ttc	tatte	tg (gggg	gtgggg	2002
	tggg	ggcag	gga (cagc	aagg	gg ga	agga	ttggg	g aag	gacaa	atag	cag	gcate	gct	gggg	atgcgg	2062
	tggg	gctc	tat (ggct [.]	tctg	ag go	egga	aagaa	a cca	agtg	gcgg	taa	tacg	gtt	atcc	acagaa	2122
	tcag	gggg	ata a	acgc	agga	aa ga	aaca	tgtga	a gca	aaaa	ggcc	agca	aaaa	ggc	cagg	aaccgt	2182
	aaaa	aagge	ccg	cgtt	gctg	gc g	tttt	tccat	t ag	gctc	cgcc	ccc	tga	cga (gcate	cacaaa	2242
	aato	gac	gct	caag [.]	tcag	ag g	tggc	gaaa	cc	gaca	ggac	tata	aaaga	ata	ccag	gcgttt	2302
	ccc	cctg	gaa (gctc	cctc	gt g	gct	ctcc	t gt	tccg	accc	tgc	gct	tac	cgga [.]	tacctg	2362
	tcc	gcct	ttc ·	tccc	ttcg	gg a	agcg [.]	tggc	g ct	ttct	cata	gct	cacg	ctg	tagg	tatctc	2422
	agti	tcgg [.]	tgt a	aggt	cgtt	cg c	tcca	agct	g gg	ctgt	gtgc	acg	aacc	ccc	cgtt	cagccc	2482
	gaco	cgct	gcg	cctt	atcc	gg ta	aact	atcg	t ct	tgag [.]	tcca	acc	cggt	aag	acac	gactta	2542
	tcg	ccac	tgg (cagc	agcc	ac t	ggta	acag	g at	tagc	agag	cga Page	ggta ! 7	tgt	aggc	ggtgct	2602

acagagttct	tgaagtggtg	gcctaactac	ggctacacta	gaaggacagt	atttggtatc	2662
tgcgctctgc	tgaagccagt	taccttcgga	aaaagagttg	gtagctcttg	atccggcaaa	2722
caaaccaccg	ctggtagcgg	tggtttttt	gtttgcaagc	agcagattac	gcgcagaaaa	2782
aaaggatctc	aagaagatcc	tttgatcttt	tctacggggt	ctgacgctca	gtggaacgaa	2842
aactcacgtt	aagggatttt	ggtcatgaga	ttatcaaaaa	ggatcttcac	ctagatcctt	2902
ttaaattaaa	aatgaagttt	taaatcaatc	taaagtatat	atgagtaacc	tgaggctatg	2962
gcagggcctg	ccgccccgac	gttggctgcg	agccctgggc	cttcacccga	acttgggggg	3022
tggggtgggg	aaaaggaaga	aacgcgggcg	tattggcccc	aatggggtct	cggtggggta	3082
tcgacagagt	gccagccctg	ggaccgaacc	ccgcgtttat	gaacaaacga	cccaacaccg	3142
tgcgttttat	tctgtctttt	tattgccgtc	atagcgcggg	ttccttccgg	tattgtctcc	3202
ttccgtgttt	cagttagcct	ccccctaggg	tgggcgaaga	actccagcat	gagatccccg	3262
cgctggagga	tcatccagcc	ggcgtcccgg	aaaacgattc	cgaagcccaa	cctttcatag	3322
aaggcggcgg	tggaatcgaa	atctcgtgat	ggcaggttgg	gcgtcgcttg	gtcggtcatt	3382
tcgaacccca	gagtcccgct	cagaagaact	cgtcaagaag	gcgatagaag	gcgatgcgct	3442
gcgaatcggg	agcggcgata	ccgtaaagca	cgaggaagcg	gtcagcccat	tcgccgccaa	3502
gctcttcagc	aatatcacgg	gtagccaacg	ctatgtcctg	atagcggtcc	gccacaccca	3562
gccggccaca	gtcgatgaat	ccagaaaagc	ggccattttc	caccatgata	ttcggcaagc	3622
aggcatcgcc	atgggtcacg	acgagatcct	cgccgtcggg	catgctcgcc	ttgagcctgg	3682
cgaacagttc	ggctggcgcg	agcccctgat	gctcttgatc	atcctgatcg	acaagaccgg	3742
cttccatccg	agtacgtgct	cgctcgatgc	gatgtttcgc	ttggtggtcg	aatgggcagg	3802
tagccggatc	aagcgtatgc	agccgccgca	ttgcatcagc	catgatggat	actttctcgg	3862
caggagcaag	gtgagatgac	aggagatcct	gccccggcac	ttcgcccaat	agcagccagt	3922
cccttcccgc	ttcagtgaca	acgtcgagca	cagctgcgca	aggaacgccc	gtcgtggcca	3982
gccacgatag	ccgcgctgcc	tcgtcttgca	gttcattcag	ggcaccggac	aggtcggtct	4042
tgacaaaaag	aaccgggcgc	ccctgcgctg	acagccggaa	cacggcggca	tcagagcagc	4102
cgattgtctg	ttgtgcccag	tcatagccga	atagcctctc	cacccaagcg	gccggagaac	4162
ctgcgtgcaa	tccatcttgt	tcaatcatgc	gaaacgatcc	tcatcctgtc	tcttgatcga	4222
tctttgcaaa	agcctaggcc	tccaaaaaag	cctcctcact	acttctggaa	tagctcagag	4282
gccgaggagg	cggcctcggc	ctctgcataa	ataaaaaaaa	ttagtcagcc	atggggcgga	4342
gaatgggcgg	aactgggcgg	agttaggggc	gggatgggcg	gagttagggg	cgggactatg	4402
gttgctgact	aattgagatg	catgctttgc	atacttctgc	ctgctgggga	gcctggggac	4462
tttccacacc	tggttgctga	ctaattgaga	tgcatgcttt	gcatacttct	gcctgctggg	4522
gagcctgggg	actttccaca	ccctaactga	cacacattcc	acagctggtt	ctttccgcct	4582
caggactctt	cctttttcaa	taaatcaatc	taaagtatat	atgagtaaac	ttggtctgac	4642
agttaccaat	gcttaatcag	tgaggcacct	atctcagcga	tctgtctatt Page 8	tcgttcatcc	4702

atagttgcct	gactccccgt	cgtgtagata	actacgatac	gggagggctt	accatctggc	4762
cccagtgctg	caatgatacc	gcgagaccca	cgctcaccgg	ctccagattt	atcagcaata	4822
aaccagccag	ccggaagggc	cgagcgcaga	agtggtcctg	caactttatc	cgcctccatc	4882
cagtctatta	attgttgccg	ggaagctaga	gtaagtagtt	cgccagttaa	tagtttgcgc	4942
aacgttgttg	ccattgctac	aggcatcgtg	gtgtcacgct	cgtcgtttgg	tatggcttca	5002
ttcagctccg	gttcccaacg	atcaaggcga	gttacatgat	ccccatgtt	gtgcaaaaaa	5062
gcggttagct	ccttcggtcc	tccgatcgtt	gtcagaagta	agttggccgc	agtgttatca	5122
ctcatggtta	tggcagcact	gcataattct	cttactgtca	tgccatccgt	aagatgcttt	5182
tctgtgactg	gtgagtactc	aaccaagtca	ttctgagaat	agtgtatgcg	gcgaccgagt	5242
tgctcttgcc	cggcgtcaat	acgggataat	accgcgccac	atagcagaac	tttaaaagtg	5302
ctcatcattg	gaaaacgttc	ttcggggcga	aaactctcaa	ggatcttacc	gctgttgaga	5362
tccagttcga	tgtaacccac	tcgtgcaccc	aactgatctt	cagcatcttt	tactttcacc	5422
agcgtttctg	ggtgagcaaa	aacaggaagg	caaaatgccg	caaaaaaggg	aataagggcg	5482
acacggaaat	gttgaatact	catactcttc	ctttttcaat	attattgaag	catttatcag	5542
ggttattgtc	tcatgagcgg	atacatattt	gaatgtattt	agaaaaataa	acaaataggg	5602
gttccgcgca	catttccccg	aaaagtgcca	cctgacgcgc	cctgtagcgg	cgcattaagc	5662
gcggcgggtg	tggtggttac	gcgcagcgtg	accgctacac	ttgccagcgc	cctagcgccc	5722
gctcctttcg	ctttcttccc	ttcctttctc	gccacgttcg	ccggctttcc	ccgtcaagct	5782
ctaaatcggg	ggctcccttt	agggttccga	tttagtgctt	tacggcacct	cgaccccaaa	5842
aaacttgatt	agggtgatgg	ttcacgtagt	gggccatcgc	cctgatagac	ggtttttcgc	5902
cctttgacgt	tggagtccac	gttctttaat	agtggactct	tgttccaaac	tggaacaaca	5962
ctcaacccta	tctcggtcta	ttcttttgat	ttataaggga	ttttgccgat	ttcggcctat	6022
tggttaaaaa	atgagctgat	ttaacaaaaa	tttaacgcga	attttaacaa	aatattaacg	6082
cttacaattt	ac .					6094

```
<210> 4
     367
```

Thr Gln Thr Arg Ala Gly Ala Gln Lys Glu Lys Thr Pro Glu Glu Pro $20 \\ 25 \\ 30$

Lys Glu Glu Val Thr Ile Lys Ala Asn Leu Ile Tyr Ala Asp Gly Lys 35 40 45 Page 9

<212> PRT <213> Artificial Sequence

<220> <223> Synthetic Construct

<400> 4

Thr Gln Thr Ala Glu Phe Lys Gly Thr Phe Glu Glu Ala Thr Ala Glu
50 60 Ala Tyr Arg Tyr Ala Asp Ala Leu Lys Lys Asp Asn Gly Glu Tyr Thr 65 70 75 Val Asp Val Ala Asp Lys Gly Tyr Thr Leu Asn Ile Lys Phe Ala Gly $85 \hspace{1cm} 90 \hspace{1cm} 95$ Lys Glu Lys Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Ala $100 \hspace{1cm} 105 \hspace{1cm} 110$ Asn Leu Ile Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly 115 120 Thr Phe Glu Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Ala Leu 130 135 140 Lys Lys Asp Asn Gly Glu Tyr Thr Val Asp Val Ala Asp Lys Gly Tyr 145 150 160 Thr Leu Asn Ile Lys Phe Ala Gly Lys Glu Lys Thr Pro Glu Glu Pro 165 170 175 Lys Glu Glu Val Thr Ile Lys Ala Asn Leu Ile Tyr Ala Asp Gly Lys 180 185 190 Thr Gln Thr Ala Glu Phe Lys Gly Thr Phe Glu Glu Ala Thr Ala Glu 195 200 205 Ala Tyr Arg Tyr Ala Asp Ala Leu Lys Lys Asp Asn Gly Glu Tyr Thr $210 \\ \hspace{1.5cm} 215 \\ \hspace{1.5cm} 220$ Val Asp Val Ala Asp Lys Gly Tyr Thr Leu Asn Ile Lys Phe Ala Gly 225 230 240 Lys Glu Lys Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Ala 245 250 255 Asn Leu Ile Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly 260 265 270Thr Phe Glu Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Ala Leu 275 280 285 Lys Lys Asp Asn Gly Glu Tyr Thr Val Asp Val Ala Asp Lys Gly Tyr Thr Leu Asn Ile Lys Phe Ala Gly Ala Ala Glu Gln Lys Leu Ile 305 310 315 320 4121-126_third_submission.ST25 Ser Glu Glu Asp Leu Asn Gly Ala Val Asp Gly Gln Asn Asp Thr Ser 325 330 335

Gln Thr Ser Ser Pro Ser Ala Ser Ser Asn Ile Ser Gly Gly Ile Phe 340 345

Leu Phe Phe Val Ala Asn Ala Ile Ile His Leu Phe Cys Phe Ser 365 365

<210> 5
<211> 5729
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic Sequence
<220>
<221> CDS
<221> CDS
<222> (682)..(1431)
<400> 5
geography acattoatta tigactagit attaatagia atg

60 gcgcgcgttg acattgatta ttgactagtt attaatagta atcaattacg gggtcattag ttcatagccc atatatggag ttccgcgtta cataacttac ggtaaatggc ccgcctggct 120 180 gaccgcccaa cgacccccgc ccattgacgt caataatgac gtatgttccc atagtaacgc 240 caatagggac tttccattga cgtcaatggg tggactattt acggtaaact gcccacttgg 300 cagtacatca agtgtatcat atgccaagta cgccccctat tgacgtcaat gacggtaaat 360 ggcccgcctg gcattatgcc cagtacatga ccttatggga ctttcctact tggcagtaca 420 tctacgtatt agtcatcgct attaccatgg tgatgcggtt ttggcagtac atcaatgggc 480 gtggatagcg gtttgactca cggggatttc caagtctcca ccccattgac gtcaatggga 540 gtttgttttg gcaccaaaat caacgggact ttccaaaatg tcgtaacaac tccgccccat 600 tgacgcaaat gggcggtagg cgtgtacggt gggaggtcta tataagcaga gctctctggc 660 taactagaga acccactgct tactggctta tcgaaattaa tacgactcac tatagggaga cccaagcttg gtaccggtgc g atg gca ccc tgc atg ctg ctc ctg ctg ttg
Met Ala Pro Cys Met Leu Leu Leu Leu
1 5 711 gcg gcc gcc ctg gcc ccg act cag acc cgc gcg ggg gcc caa aag ccc Ala Ala Ala Leu Ala Pro Thr Gln Thr Arg Ala Gly Ala Gln Lys Pro 15 20 25759 gag gtg atc gat gcc agc gag ctg acc ccc gcc gtg acc acc tac aag Glu Val Ile Asp Ala Ser Glu Leu Thr Pro Ala Val Thr Thr Tyr Lys 30 40807 gtg atc aac ggc aag acc ctg aag ggc gag acc acc acc gag gcc Val Ile Asn Gly Lys Thr Leu Lys Gly Glu Thr Thr Thr Glu Ala 45 50 55 855 903 gtg gac gcc gcc acc gcg gag aag gtg ttc aaa caa tac gct aat gac Val Asp Ala Ala Thr Ala Glu Lys Val Phe Lys Gln Tyr Ala Asn Asp 60 65 70aac ggg gtc gac ggc gag tgg act tac gac gac gcc acc aag acc ttc Asn Gly Val Asp Gly Glu Trp Thr Tyr Asp Asp Ala Thr Lys Thr Phe 951

Page 11

75					80			4121	-126	_thi 85	rd_s	ubmi	ssio	n.ST	25 90	
acc Thr	gtg Val	acc Thr	gag Glu	aag Lys 95	ccc Pro	gag Glu	gtg Val	atc Ile	gat Asp 100	gcc Ala	agc Ser	gag Glu	ctg Leu	acc Thr 105	ccc Pro	999
gcc Ala	gtg Val	acc Thr	acc Thr 110	tac Tyr	aag Lys	cta Leu	gtg Val	atc Ile 115	aac Asn	ggc Gly	aag Lys	acc Thr	ctg Leu 120	aag Lys	ggc Gly	1047
gag Glu	acc Thr	acc Thr 125	acc Thr	gag Glu	gcc Ala	gtg val	gac Asp 130	gcc Ala	gcc Ala	acc Thr	gcg Ala	gag Glu 135	aag Lys	gtg Val	ttc Phe	1095
aaa Lys	caa Gln 140	tac Tyr	gct Ala	aat Asn	gac Asp	aac Asn 145	ggg Gly	gtc val	gac Asp	ggc Gly	gag Glu 150	tgg Trp	act Thr	tac Tyr	gac Asp	1143
gac Asp 155	gcc Ala	acc Thr	aag Lys	acc Thr	ttc Phe 160	acc Thr	gtg Val	acc Thr	gag Glu	gcg Ala 165	gcc Ala	gca Ala	gaa Glu	caa Gln	aaa Lys 170	1191
ctc Leu	atc Ile	tca Ser	gaa Glu	gag Glu 175	gat Asp	ctg Leu	aat Asn	ggg Gly	gcc Ala 180	gtc Val	gac Asp	gaa Glu	caa Gln	aaa Lys 185	ctc Leu	1239
atc Ile	tca Ser	gaa Glu	gag Glu 190	gat Asp	ctg Leu	aat Asn	gct Ala	gtg Val 195	ggc Gly	cag Gln	gac Asp	acg Thr	cag Gln 200	gag Glu	gtc Val	1287
atc Ile	gtg val	gtg Val 205	cca Pro	cac His	tcc Ser	ttg Leu	ccc Pro 210	ttt Phe	aag Lys	gtg Val	gtg Val	gtg Val 215	atc Ile	tca Ser	gcc Ala	1335
atc Ile	ctg Leu 220	gcc Ala	ctg Leu	gtg val	gtg val	ctc Leu 225	acc Thr	atc Ile	atc Ile	tcc Ser	ctt Leu 230	atc Ile	atc Ile	ctc Leu	atc Ile	1383
atg Met 235	ctt Leu	tgg Trp	cag Gln	aag Lys	aag Lys 240	cca Pro	cgt Arg	tcg Ser	tcg Ser	gcc Ala 245	gat Asp	cga Arg	gaa Glu	tcc Ser	atc Ile 250	1431
taga	agcta	att (ctata	agtgi	tc ac	cta	aatgo	tag	gagct	cgc	tgat	tcago	cct	cgact	tgtgcc	1491
ttct	agti	tgc (cagco	catc	tg ti	tgtt	tgcc	cto	cccc	gtg	cct1	tccti	tga (ccct	ggaagg	1551
tgc	acto	cc a	actgi	tcct1	tt co	taat	taaaa	a tga	aggaa	aatt	gcat	tcgca	att 🤉	gtct	gagtag	1611
gtgi	cati	tct a	attci	tgggg	gg g1	tggg	gtgg	g gca	agga	agc	aagg	gggga	agg a	attg	ggaaga	1671
caat	agca	agg (catgo	tgg	gg at	tgcg	gtgg	gcto	ctate	gct	tct	gagge	cgg a	aaaga	aaccag	1731
tgg	ggta	aat a	acggt	ttato	cc ac	cagaa	atca	g gg(gataa	acgc	agga	aaaga	aac a	atgt	gagcaa	1791
aagg	gccag	gca a	aaag	gccag	gg aa	accg	taaaa	a agg	gccg	gtt	gct	ggcgt	ttt	ttcc	ataggc	1851
tcc	gccc	ccc 1	tgac	gagca	at ca	acaa	aaat	c gad	gct	aag	tcag	gaggt	tgg (cgaa	acccga	1911
cag	gacta	ata a	aagat	tacca	ag go	gtt	tccc	ct	ggaag	gctc	cct	cgtg	cgc 1	tctc	ctgttc	1971
cga	cct	gcc (gctta	accg	ga ta	acct	gtcc	g cc	tttc	tccc	ttc	ggga	agc (gtgg	cgcttt	2031
ctca	atago	ctc a	acgci	tgtag	gg ta	atct	cagt	t cg	gtgta	aggt	cgti	tcgc	tcc a	aagc	tgggct	2091
gtg	tgcad	cga a	accc	cccg	tt ca	agcc	cgac	c gc1	tgcg	ctt	atc	cggta	aac ·	tatc	gtcttg	2151
agt	caa	ccc (ggta	agaca	ac ga	actt	atcg	c ca	ctgg	cagc	agc	cact	ggt	aaca	ggatta	2211
gcag	gagc	gag (gtat	gtag	gc gg	gtgc	taca	g ag	ttct	tgaa	gtg	gtgg	cct	aact	acggct	2271

acactagaag	gacagtattt	4 ggtatctgcg	121-126_thi ctctgctgaa	rd_submissi gccagttacc	on.ST25 ttcggaaaaa	2331
gagttggtag	ctcttgatcc	ggcaaacaaa	ccaccgctgg	tagcggtggt	ttttttgttt	2391
gcaagcagca	gattacgcgc	agaaaaaaag	gatctcaaga	agatcctttg	atcttttcta	2451
cggggtctga	cgctcagtgg	aacgaaaact	cacgttaagg	gattttggtc	atgagattat	2511
caaaaaggat	cttcacctag	atccttttaa	attaaaaatg	aagttttaaa	tcaatctaaa	2571
gtatatatga	gtaacctgag	gctatggcag	ggcctgccgc	cccgacgttg	gctgcgagcc	2631
ctgggccttc	acccgaactt	ggggggtggg	gtggggaaaa	ggaagaaacg	cgggcgtatt	2691
ggccccaatg	gggtctcggt	ggggtatcga	cagagtgcca	gccctgggac	cgaaccccgc	2751
gtttatgaac	aaacgaccca	acaccgtgcg	ttttattctg	tctttttatt	gccgtcatag	2811
cgcgggttcc	ttccggtatt	gtctccttcc	gtgtttcagt	tagcctcccc	ctagggtggg	2871
cgaagaactc	cagcatgaga	tcccgcgct	ggaggatcat	ccagccggcg	tcccggaaaa	2931
cgattccgaa	gcccaacctt	tcatagaagg	cggcggtgga	atcgaaatct	cgtgatggca	2991
ggttgggcgt	cgcttggtcg	gtcatttcga	accccagagt	cccgctcaga	agaactcgtc	3051
aagaaggcga	tagaaggcga	tgcgctgcga	atcgggagcg	gcgataccgt	aaagcacgag	3111
gaagcggtca	gcccattcgc	cgccaagctc	ttcagcaata	tcacgggtag	ccaacgctat	3171
gtcctgatag	cggtccgcca	cacccagccg	gccacagtcg	atgaatccag	aaaagcggcc	3231
attttccacc	atgatattcg	gcaagcaggc	atcgccatgg	gtcacgacga	gatcctcgcc	3291
gtcgggcatg	ctcgccttga	gcctggcgaa	cagttcggct	ggcgcgagcc	cctgatgctc	3351
ttgatcatcc	tgatcgacaa	gaccggcttc	catccgagta	cgtgctcgct	cgatgcgatg	3411
tttcgcttgg	tggtcgaatg	ggcaggtagc	cggatcaagc	gtatgcagcc	gccgcattgc	3471
atcagccatg	atggatactt	tctcggcagg	agcaaggtga	gatgacagga	gatcctgccc	3531
cggcacttcg	cccaatagca	gccagtccct	tcccgcttca	gtgacaacgt	cgagcacagc	3591
tgcgcaagga	acgcccgtcg	tggccagcca	cgatagccgc	gctgcctcgt	cttgcagttc	3651
attcagggca	ccggacaggt	cggtcttgac	aaaaagaacc	gggcgcccct	gcgctgacag	3711
ccggaacacg	gcggcatcag	agcagccgat	tgtctgttgt	gcccagtcat	agccgaatag	3771
cctctccacc	caagcggccg	gagaacctgc	gtgcaatcca	tcttgttcaa	tcatgcgaaa	3831
cgatcctcat	cctgtctctt	gatcgatctt	tgcaaaagcc	taggcctcca	aaaaagcctc	3891
ctcactactt	ctggaatagc	tcagaggccg	aggaggcggc	ctcggcctct	gcataaataa	3951
aaaaaattag	tcagccatgg	ggcggagaat	gggcggaact	gggcggagtt	aggggcggga	4011
tgggcggagt	taggggcggg	actatggttg	ctgactaatt	gagatgcatg	ctttgcatac	4071
ttctgcctgc	tggggagcct	ggggactttc	cacacctggt	tgctgactaa	ttgagatgca	4131
tgctttgcat	acttctgcct	gctggggagc	ctggggactt	tccacaccct	aactgacaca	4191
cattccacag	ctggttcttt	ccgcctcagg	actcttcctt	tttcaataaa	tcaatctaaa	4251
gtatatatga	gtaaacttgg	tctgacagtt	accaatgctt	aatcagtgag	gcacctatct	4311
cagcgatctg	tctatttcgt	tcatccatag	ttgcctgact	ccccgtcgtg	tagataacta	4371

castscagas	agacttacca	4 tctggcccca	121-126_thi	rd_submissi	on.ST25	4431
						4491
caccggctcc	agatttatca	gcaataaacc	agccagccgg	aagggccgag	cgcagaagtg	
gtcctgcaac	tttatccgcc	tccatccagt	ctattaattg	ttgccgggaa	gctagagtaa	4551
gtagttcgcc	agttaatagt	ttgcgcaacg	ttgttgccat	tgctacaggc	atcgtggtgt	4611
cacgctcgtc	gtttggtatg	gcttcattca	gctccggttc	ccaacgatca	aggcgagtta	4671
catgatcccc	catgttgtgc	aaaaaagcgg	ttagctcctt	cggtcctccg	atcgttgtca	4731
gaagtaagtt	ggccgcagtg	ttatcactca	tggttatggc	agcactgcat	aattctctta	4791
ctgtcatgcc	atccgtaaga	tgcttttctg	tgactggtga	gtactcaacc	aagtcattct	4851
gagaatagtg	tatgcggcga	ccgagttgct	cttgcccggc	gtcaatacgg	gataataccg	4911
cgccacatag	cagaacttta	aaagtgctca	tcattggaaa	acgttcttcg	gggcgaaaac	4971
tctcaaggat	cttaccgctg	ttgagatcca	gttcgatgta	acccactcgt	gcacccaact	5031
gatcttcagc	atcttttact	ttcaccagcg	tttctgggtg	agcaaaaaca	ggaaggcaaa	5091
atgccgcaaa	aaagggaata	agggcgacac	ggaaatgttg	aatactcata	ctcttccttt	5151
ttcaatatta	ttgaagcatt	tatcagggtt	attgtctcat	gagcggatac	atatttgaat	5211
gtatttagaa	aaataaacaa	ataggggttc	cgcgcacatt	tccccgaaaa	gtgccacctg	5271
acgcgccctg	tagcggcgca	ttaagcgcgg	cgggtgtggt	ggttacgcgc	agcgtgaccg	5331
ctacacttgc	cagcgcccta	gcgcccgctc	ctttcgcttt	cttcccttcc	tttctcgcca	5391
cgttcgccgg	ctttccccgt	caagctctaa	atcgggggct	ccctttaggg	ttccgattta	5451
gtgctttacg	gcacctcgac	cccaaaaaac	ttgattaggg	tgatggttca	cgtagtgggc	5511
catcgccctg	atagacggtt	tttcgccctt	tgacgttgga	gtccacgttc	tttaatagtg	5571
gactcttgtt	ccaaactgga	acaacactca	accctatctc	ggtctattct	tttgatttat	5631
aagggatttt	gccgatttcg	gcctattggt	taaaaaatga	gctgatttaa	caaaaattta	5691
acgcgaattt	taacaaaata	ttaacgctta	caatttac			5729

```
<210> 6
<211> 250
```

<220> <223> Synthetic Construct

<400> 6

Met Ala Pro Cys Met Leu Leu Leu Leu Leu Ala Ala Ala Leu Ala Pro 1 5 10 15

Thr Gln Thr Arg Ala Gly Ala Gln Lys Pro Glu Val Ile Asp Ala Ser 20 25 30

Glu Leu Thr Pro Ala Val Thr Thr Tyr Lys Leu Val Ile Asn Gly Lys $35 \hspace{1cm} 40 \hspace{1cm} 45$

Thr Leu Lys Gly Glu Thr Thr Glu Ala Val Asp Ala Ala Thr Ala Page 14

<212> PRT <213> Artificial Sequence

Glu Lys Val Phe Lys Gln Tyr Ala Asn Asp Asn Gly Val Asp Gly Glu 65 70 75 Trp Thr Tyr Asp Asp Ala Thr Lys Thr Phe Thr Val Thr Glu Lys Pro

Glu Val Ile Asp Ala Ser Glu Leu Thr Pro Ala Val Thr Thr Tyr Lys $100 \hspace{1.5cm} 105 \hspace{1.5cm} 110$

Leu Val Ile Asn Gly Lys Thr Leu Lys Gly Glu Thr Thr Glu Ala 115 120

Val Asp Ala Ala Thr Ala Glu Lys Val Phe Lys Gln Tyr Ala Asn Asp 130 140

Asn Gly Val Asp Gly Glu Trp Thr Tyr Asp Asp Ala Thr Lys Thr Phe 145 150 155 160

Thr Val Thr Glu Ala Ala Ala Glu Gln Lys Leu Ile Ser Glu Glu Asp 165 170

Leu Asn Gly Ala Val Asp Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu 180 185 190

Asn Ala Val Gly Gln Asp Thr Gln Glu Val Ile Val Val Pro His Ser 195 200 205

Leu Pro Phe Lys Val Val Ile Ser Ala Ile Leu Ala Leu Val Val 210 215 220

Leu Thr Ile Ile Ser Leu Ile Ile Leu Ile Met Leu Trp Gln Lys Lys 225 230 235 240

Pro Arg Ser Ser Ala Asp Arg Glu Ser Ile 245 250

262

<211> <212> PRT

Artificial Sequence

<220> <223>

Synthetic Construct

<400>

met Ile Glu Gln Asp Gly Leu His Ala Gly Ser Pro Ala Ala Trp Val 1 5 10

Glu Arg Leu Phe Gly Tyr Asp Trp Ala Gln Gln Thr Ile Gly Cys Ser 20 30

Asp Ala Ala Val Phe Arg Leu Ser Ala Gln Gly Arg Pro Val Leu Phe

Val Lys Thr Asp Leu Ser Gly Ala Leu Asn Glu Leu Gln Asp Glu Ala 50 60 Ala Arg Leu Ser Trp Leu Ala Thr Thr Gly Val Pro Cys Ala Ala Val 65 70 75 80 Leu Asp Val Val Thr Glu Ala Gly Arg Asp Trp Leu Leu Leu Gly Glu 85 90 95 Val Pro Gly Gln Asp Leu Leu Ser Ser His Leu Ala Pro Ala Glu Lys 100 110 Val Ser Ile Met Ala Asp Ala Met Arg Arg Leu His Thr Leu Asp Pro 115 120 125 Ala Thr Cys Pro Phe Asp His Gln Ala Lys His Arg Ile Glu Arg Ala 130 135 140 Arg Thr Arg Met Glu Ala Gly Leu Val Asp Gln Asp Gln Glu His 145 150 160 Gln Gly Leu Ala Pro Ala Glu Leu Phe Ala Arg Leu Lys Ala Ser Met 165 170 175 Pro Asp Gly Glu Asp Leu Val Val Thr His Gly Asp Ala Cys Leu Pro 180 185 Asn Ile Met Val Glu Asn Gly Arg Phe Ser Gly Phe Ile Asp Cys Gly 195 200 205 Arg Leu Gly Val Ala Asp Arg Tyr Gln Asp Ile Ala Leu Ala Thr Arg 210 220 Asp Ile Ala Glu Glu Leu Gly Gly Glu Trp Ala Asp Arg Phe Leu Val 225 230 240 Leu Tyr Gly Ile Ala Ala Pro Asp Ser Gln Arg Ile Ala Phe Tyr Arg 245 250 255

Leu Leu Asp Glu Phe Phe 260

<400>

Met Ser Ile Gln His Phe Arg Val Ala Leu Ile Pro Phe Phe Ala Ala Page 16

<210> 286

<211> <212> PRT

Artificial Sequence

<220> <223> Synthetic Construct

Phe Cys Leu Pro Val Phe Ala His Pro Glu Thr Leu Val Lys Val Lys 20 25 30 Asp Ala Glu Asp Gln Leu Gly Ala Arg Val Gly Tyr Ile Glu Leu Asp 45 Leu Asn Ser Gly Lys Ile Leu Glu Ser Phe Arg Pro Glu Glu Arg Phe 50 60 Pro Met Met Ser Thr Phe Lys Val Leu Leu Cys Gly Ala Val Leu Ser 65 70 75 80 Arg Ile Asp Ala Gly Gln Glu Gln Leu Gly Arg Arg Ile His Tyr Ser Gln Asn Asp Leu Val Glu Tyr Ser Pro Val Thr Glu Lys His Leu Thr $100 \hspace{1cm} 105 \hspace{1cm} 110$ Asp Gly Met Thr Val Arg Glu Leu Cys Ser Ala Ala Ile Thr Met Ser 115 120 125 Asp Asn Thr Ala Ala Asn Leu Leu Leu Thr Thr Ile Gly Gly Pro Lys 130 135 140 Glu Leu Thr Ala Phe Leu His Asn Met Gly Asp His Val Thr Arg Leu 145 150 160 Asp Arg Trp Glu Pro Glu Leu Asn Glu Ala Ile Pro Asn Asp Glu Arg 165 170 175 Asp Thr Thr Met Pro Val Ala Met Ala Thr Thr Leu Arg Lys Leu Leu 180 185 190 Thr Gly Glu Leu Leu Thr Leu Ala Ser Arg Gln Gln Leu Ile Asp Trp 195 200 205 Met Glu Ala Asp Lys Val Ala Gly Pro Leu Leu Arg Ser Ala Leu Pro 210 215 220 Ala Gly Trp Phe Ile Ala Asp Lys Ser Gly Ala Gly Glu Arg Gly Ser 225 230 235 240 Arg Gly Ile Ile Ala Ala Leu Gly Pro Asp Gly Lys Pro Ser Arg Ile 245 250 255 Val Val Ile Tyr Thr Gly Ser Gln Ala Thr Met Asp Glu Arg Asn 260 265 Arg Gln Ile Ala Glu Ile Gly Ala Ser Leu Ile Lys His Trp 285